garabedian1.1A.ST25.txt

SEQUENCE LISTING

<110> GARABEDIAN, Michael
      TANEJA, Samir
      HITTELMAN, Adam
      MARKUS, Steven

<120> METHOD FOR SCREENING TRANSCRIPTIONAL COREGULATORY PROTEINS OF TRANSCR
IPTION FACTORS, AND ANDROGEN RECEPTOR TRANSCRIPTIONAL COREGULATORY PROTEINS
AS TARGETS FOR ANDROGEN RECEPTOR-DEPENDENT DISEASES

<130> GARABEDIAN=1.1A

<140> 09/816,669
<141> 2001-03-26

<150> 60/225,618
<151> 2000-08-15

<150> 60/191,768
<151> 2000-03-24

<160> 20

<170> PatentIn version 3.1

<210> 1
<211> 474
<212> DNA
<213> human

<400> 1
atggcgacgc cccctaagcg gcgggcggtg gaggccacgg gggagaaagt gctgcgctac      60

gagaccttca tcagtgacgt gctgcagcgg gacttgcgaa aggtgctgga ccatcgagac     120

aaggtatatg agcagctggc caaatacctt caactgagaa atgtcattga gcgactccag     180

gaagctaagc actcggagtt atatatgcag gtggatttgg gctgtaactt cttcgttgac     240

acagtggtcc cagatacttc acgcatctat gtggccctgg gatatggttt tttcctggag     300

ttgacactgg cagaagctct caagttcatt gatcgtaaga gctctctcct cacagagctc     360

agcaacagcc tcaccaagga ctccatgaat atcaaagccc atatccacat gttgctagag     420

gggcttagag aactacaagg cctgcagaat ttcccagaga agcctcacca ttga            474

<210> 2
<211> 157
<212> PRT
<213> human

<400> 2

Met Ala Thr Pro Pro Lys Arg Arg Ala Val Glu Ala Thr Gly Glu Lys
1               5                   10                  15


Val Leu Arg Tyr Glu Thr Phe Ile Ser Asp Val Leu Gln Arg Asp Leu
            20                  25                  30

Page 1

```
Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr Glu Gln Leu Ala Lys
         35              40              45

Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu Gln Glu Ala Lys His
     50              55              60

Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys Asn Phe Phe Val Asp
65              70              75              80

Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val Ala Leu Gly Tyr Gly
             85              90              95

Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu Lys Phe Ile Asp Arg
             100             105             110

Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser Leu Thr Lys Asp Ser
         115             120             125

Met Asn Ile Lys Ala His Ile His Met Leu Leu Glu Gly Leu Arg Glu
     130             135             140

Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro His His
145             150             155
```

```
<210>  3
<211>  1097
<212>  DNA
<213>  human

<400>  3
aaatgcacaa cccggacgga agtgcctctc cgacagcaga tccaggctcg gagctccaga      60

cgctgggaca ggccgcccgc agaccacccc cgccgcgcgc gggacacgac gccccccgca     120

ggacacgccc atcagcccgg aaacccctga gctgcttctc ccggaggccg atgcccaccc     180

gggagccccc aaagactcgc ggctcccggg ggcacctgca tactcacccg cctgggcctg     240

ggcccccgct gcagggactg gcgccccgag gcctcaaaac cagcgccccc cgccctccgt     300

gccagcccca gccgggaccc cacaaggcaa agaccaagaa gattgtgttt gaggatgagt     360

tgctctccca ggccctcctg ggcgccaaga agcctattgg agccatccct aaggggcata     420

agcctaggcc ccacccagtg cccgactatg agcttaagta cccgccagtg agcagtgaga     480

gggaacggag ccgctatgtc gcagtgttcc aggaccagta cggagagttc ttggagctcc     540

agcacgaggt ggggtgtgca caggcaaagc tcaggcagct ggaggccctg ctgagctccc     600

tgcccccacc ccaaagccag aaggaggccc aagttgcagc ccgggtttgg agggagtttg     660

agatgaagcg aatggatcct ggcttcctgg acaagcaggc tcgctgccac tacctgaagg     720
```

```
gtaaactgag gcatctcaag actcagatcc agaaattcga tgaccaagga gacagcgagg        780

gctccgtgta cttctaagtg cccctgcaga tgggcagagg gatgcatggg gatgcaggtc        840

ccttgcattt cttggtatct ctcagctttt cctcttgcag ctccccctac caggggtcgc        900

tttctcctgg attgcaaatg cctcttcagt ttggactcag ctctgacagc ccctcctcca        960

ggaaggcctt ccaggacttc ctcctctggg tcctctagct ctgaccctac agggactcca       1020

gatctcaacc tgttccctgg aagtagggcc tgctctccat cccagtgaaa taaacatgta       1080

ttagacacct aaaaaaa                                                      1097
```

```
<210>   4
<211>   264
<212>   PRT
<213>   Human

<400>   4
```

```
Met His Asn Pro Asp Gly Ser Ala Ser Pro Thr Ala Asp Pro Gly Ser
1               5                   10                  15


Glu Leu Gln Thr Leu Gly Gln Ala Ala Arg Arg Pro Pro Pro Pro Arg
            20                  25                  30


Ala Gly His Asp Ala Pro Arg Arg Thr Arg Pro Ser Ala Arg Lys Pro
            35                  40                  45


Leu Ser Cys Phe Ser Arg Arg Pro Met Pro Thr Arg Glu Pro Pro Lys
        50                  55                  60


Thr Arg Gly Ser Arg Gly His Leu His Thr His Pro Pro Gly Pro Gly
65                  70                  75                  80


Pro Pro Leu Gln Gly Leu Ala Pro Arg Gly Leu Lys Thr Ser Ala Pro
                85                  90                  95


Arg Pro Pro Cys Gln Pro Gln Pro Gly Pro His Lys Ala Lys Thr Lys
                100                 105                 110


Lys Ile Val Phe Glu Asp Glu Leu Leu Ser Gln Ala Leu Leu Gly Ala
            115                 120                 125


Lys Lys Pro Ile Gly Ala Ile Pro Lys Gly His Lys Pro Arg Pro His
        130                 135                 140


Pro Val Pro Asp Tyr Glu Leu Lys Tyr Pro Pro Val Ser Ser Glu Arg
145                 150                 155                 160


Glu Arg Ser Arg Tyr Val Ala Val Phe Gln Asp Gln Tyr Gly Glu Phe
```

```
                    165                    170                    175


     Leu Glu Leu Gln His Glu Val Gly Cys Ala Gln Ala Lys Leu Arg Gln
              180                    185                    190


     Leu Glu Ala Leu Leu Ser Ser Leu Pro Pro Pro Gln Ser Gln Lys Glu
              195                    200                    205


     Ala Gln Val Ala Ala Arg Val Trp Arg Glu Phe Glu Met Lys Arg Met
          210                    215                    220


     Asp Pro Gly Phe Leu Asp Lys Gln Ala Arg Cys His Tyr Leu Lys Gly
     225                    230                    235                    240


     Lys Leu Arg His Leu Lys Thr Gln Ile Gln Lys Phe Asp Asp Gln Gly
                        245                    250                    255


     Asp Ser Glu Gly Ser Val Tyr Phe
                        260
```

```
<210>  5
<211>  517
<212>  DNA
<213>  Human

<220>
<221>  misc_feature
<222>  (65)..(65)
<223>  n at position is unknown.


<400>  5
gaacggcacg agggcgcgcc acgcgcggga agcggcgcgc ggagcgcgcg cggcgggccg     60

cgcanccgag ggagccgagc gcccgmacgc gcccgagcgg acasacgcca gagccgcgcc    120

ccgggccgag cgcagcgcgc cggccgssyg ggccgccagg ggcgcgcgcg gcggagcgcg    180

gggcgcgmga aaaggggccc ggcggagacc aagggcaggc gcggcccgca agggcgccgg    240

ggaaggcgcc cggcaaggag gcggacaagc ggagcaggcc aacgagacgc gcgcacccac    300

acacgagcgc gagccgccac aacaccacac ccggcccaag gagaacagca cgccaacgcg    360

ccagycacgg cgggcacggg aggcgggcca cacacagcgg ccccgccaag gcacggcgca    420

cggcacaagg gcaccacgcc agacaagcga ggaggcagca cgccgagacc ggccggaggg    480

ccgcgaccgc cggagaaaag gaacagagag cccccca                            517


<210>  6
<211>  189
<212>  PRT
<213>  Human
```

<400> 6

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Glu | Phe | Gly | Thr | Arg | Ala | Arg | Phe | Thr | Arg | Gly | Lys | Ser | Ala | Leu | Leu |
| 1 | | | | 5 | | | | | 10 | | | | 15 | |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Glu | Arg | Ala | Leu | Ala | Arg | Pro | Arg | Thr | Glu | Val | Ser | Leu | Ser | Ala | Phe |
| | | 20 | | | | | 25 | | | | 30 | | | |

Ala Leu Leu Ser Pro Ser Trp Tyr Ser Thr Ala Arg Ala Val Phe Ser
        35              40              45

Val Ala Glu Leu Gln Ser Arg Leu Ala Ala Leu Gly Arg Gln Val Gly
    50              55              60

Ala Arg Val Leu Asp Ala Leu Val Ala Arg Glu Lys Gly Ala Arg Arg
65              70              75              80

Glu Thr Lys Val Leu Gly Ala Leu Leu Phe Val Lys Gly Ala Val Trp
              85              90              95

Lys Ala Leu Phe Gly Lys Glu Ala Asp Lys Leu Glu Gln Ala Asn Asp
        100             105             110

Asp Ala Arg Thr Phe Tyr Ile Ile Glu Arg Glu Pro Leu Ile Asn Thr
        115             120             125

Tyr Ile Ser Val Pro Lys Glu Asn Ser Thr Leu Asn Cys Ala Ser Phe
    130             135             140

Thr Ala Gly Ile Val Glu Ala Val Leu Thr His Ser Gly Phe Pro Ala
145             150             155             160

Lys Val Thr Ala His Trp His Lys Gly Thr Thr Leu Met Ile Lys Phe
            165             170             175

Glu Glu Ala Val Ile Ala Arg Asp Arg Leu Glu Gly Arg
            180             185

<210>  7
<211>  126
<212>  DNA
<213>  Human

<400>  7
gaattcggca cgaggctcaa gccctacgtg agctacctcg cccctgagag cgaggagacg      60

cccctgacgg ccgcgcagct cttcagcaag ccgttggcgc cttgccatcg aaaaggactt     120

caagga                                                                126

```
<210>  8
<211>  42
<212>  PRT
<213>  Human

<400>  8

Glu Phe Gly Thr Arg Leu Lys Pro Tyr Val Ser Tyr Leu Ala Pro Glu
1               5                   10                  15


Ser Glu Glu Thr Pro Leu Thr Ala Ala Gln Leu Phe Ser Lys Pro Leu
            20                  25                  30


Ala Pro Cys His Arg Lys Gly Leu Gln Gly
        35                  40


<210>  9
<211>  678
<212>  DNA
<213>  Human

<220>
<221>  misc_feature
<222>  (651)..(651)
<223>  n at position is unknown.


<220>
<221>  misc_feature
<222>  (657)..(657)
<223>  n at position is unknown.


<400>  9
gaattcggca cgaggattca ttgcccccac aatcctaggc ctacccgccg cagtactgat      60

cattctattt cccctctat tgatccccac ctccaaatat ctcatcaaca accgactaat      120

caccacccaa caatgactaa tcaaactaac ctcaaaacaa atgataacca tacacaacac      180

taaaggacga acctgatctc ttatactagt atccttaatc attttattg ccacaactaa       240

cctcctcgga ctcctgcctc actcatttac accaaccacc caactatcta taaacctagc      300

catggccatc cccttatgag cgggcgcagt gattataggc tttcgctcta agattaaaaa      360

tgccctagcc cacttcttac acaaggcac acctacaccc cttatcccca tactagttat       420

tatcgaaacc atcagcctac tcattcaacc aatagccctg gccgtacgcc taaccgctaa      480

cattactgca ggccacctac tcatgcacct aattggaagc gccaccctag caatatcaac      540

cattaacctt cctctacact tatcatcttc acaattctaa ttctactgac tatcctagaa      600

atcgctgtcg ccttaatcca agcctacgtt ttcacacttc tagtaagcct ntactgnacg      660

acaacacata aaaaaaaa                                                    678


<210>  10
```

```
<211>   60
<212>   PRT
<213>   Human

<400>   10

Glu Phe Gly Thr Arg Ile His Cys Pro His Asn Pro Arg Pro Thr Arg
1               5                   10                  15


Arg Ser Thr Asp His Ser Ile Ser Pro Ser Ile Asp Pro His Leu Gln
            20                  25                  30


Ile Ser His Gln Gln Pro Thr Asn His His Pro Thr Met Thr Asn Gln
            35                  40                  45


Thr Asn Leu Lys Thr Asn Asp Asn His Thr Gln His
    50                  55                  60


<210>   11
<211>   1918
<212>   DNA
<213>   Human

<400>   11
gaattccaat gtggtaaagt cttcgctcaa acatcacaac ttgcaaggca ttggagagtt    60

catactggag aaaaacctta caagtgtaat gactgtggca gagcctttag tgatcgttca   120

agcctaactt ttcatcaggc aatacatact ggagagaaac cttacaaatg tcatgaatgc   180

ggcaaggttt ttaggcacaa ttcatacctt gcaactcatc ggcgaattca tactggagag   240

aaaccttaca agtgtaatga gtgtgggaaa gcctttagta tgcattcaaa cctaactacc   300

cataaggtca tccatactgg agagaagcct tacaaatgta atcaatgtgg caaggtcttc   360

actcagaact cacaccttgc aaatcatcaa aggactcaca ccggagagaa accttaccga   420

tgcaatgagt gtgggaaagc cttcagtgtt cgttcaagcc taaccaccca tcaggcaatc   480

catactggga aaaaacctta caaatgtaat gaatgtggca aggtctttac tcaaaatgct   540

cacctggcaa atcaccgaag aattcatact ggggagaaac cttacaggtg tacagagtgt   600

gggaaagcct ttagggtaag atcaagtcta actacccata tggcaatcca cactggagaa   660

aagcgttaca atgtaatga gtgtggcaag gtcttcaggc agagttcaaa tcttgcaagt   720

catcacagaa tgcataccgg agagaaacct tacaaatgag tgtggtgagg tcattaggta   780

caattcactc ctttcacatc agttaatttc attcttgaca gaatccttac aaatgtagtg   840

acagtggcca atccctcatg agttgaagca ttaatagata tgagaggcca taagcaagag   900

acatcatgta acatatgtg cagagggtc tatccaggcc tcgcaggtta ctaggcatca   960

agatttatat ctttgatgaa acgaaacaaa tgtaatatgc atcctgaggc cattacccag  1020

tgaccgatgg taagtgagga ttcctaggag gaataacagt ctctggtttc cctgtttgcc  1080
```

```
tttgatatta tacactgtag aatactcaca agtccaaata tgctaaaaat tatatatttt    1140

taactcacat acgaaaaggt tgcaggatat ttgtaggcag tcagttacct tcaccttatg    1200

aaatgtttca ctgagttatt tgaggttttt tggaaagcct actattgcgt ttcaatgtga    1260

actttgaaat cttattgtgc atccttacac accttccatg gtgctttctt ggaaagatca    1320

ttgggatgga aggatcattg attgggtgaa gatcattgat taggtgaagg attatttcta    1380

tccaatttgt gaagaaggag gactttgctt ttaaaattaa gtatcatctg aattagcatt    1440

tgggagtggc gaaaaacaat gtaaaactat gatgtcactc accattctga taatgttcag    1500

ggtgcctttc tcctaccagg agagtactgt ggcttagagg aaagaaatgg tctatcaact    1560

gaacatgaaa tggagcaggc caagacctta ggacattggg atttttgtgg gaggagagta    1620

ataggtaatt agacactgat tgtgtggtag aaatactgca ggggaaaagg tcgccctctt    1680

atgcatcaaa gagcaatacc tgttgtttag caagagtga tgaaaaattg atcttgtttt    1740

gaaattgaag agagaggcca ggcgcggtgg ctcacacctg taatcccagc actttgggag    1800

gctgaggcag gtggatcacc tgaggtcggg agttcgagac cagcctgacc aacatggaga    1860

aaccccaatt gtactaaaaa tacaaaatta gccgggcgtg gtggcaggtg cggaattc      1918
```

<210> 12
<211> 252
<212> PRT
<213> Human

<400> 12

```
Glu Phe Gln Cys Gly Lys Val Phe Ala Gln Thr Ser Gln Leu Ala Arg
1               5                   10                  15


His Trp Arg Val His Thr Gly Glu Lys Pro Tyr Lys Cys Asn Asp Cys
            20                  25                  30


Gly Arg Ala Phe Ser Asp Arg Ser Ser Leu Thr Phe His Gln Ala Ile
        35                  40                  45


His Thr Gly Glu Lys Pro Tyr Lys Cys His Glu Cys Gly Lys Val Phe
    50                  55                  60


Arg His Asn Ser Tyr Leu Ala Thr His Arg Arg Ile His Thr Gly Glu
65                  70                  75                  80


Lys Pro Tyr Lys Cys Asn Glu Cys Gly Lys Ala Phe Ser Met His Ser
                85                  90                  95


Asn Leu Thr Thr His Lys Val Ile His Thr Gly Glu Lys Pro Tyr Lys
            100                 105                 110
```

```
Cys Asn Gln Cys Gly Lys Val Phe Thr Gln Asn Ser His Leu Ala Asn
         115                 120             125

His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Arg Cys Asn Glu Cys
         130             135                 140

Gly Lys Ala Phe Ser Val Arg Ser Ser Leu Thr Thr His Gln Ala Ile
145                 150                 155                 160

His Thr Gly Lys Lys Pro Tyr Lys Cys Asn Glu Cys Gly Lys Val Phe
             165                 170                 175

Thr Gln Asn Ala His Leu Ala Asn His Arg Arg Ile His Thr Gly Glu
             180                 185                 190

Lys Pro Tyr Arg Cys Thr Glu Cys Gly Lys Ala Phe Arg Val Arg Ser
         195                 200                 205

Ser Leu Thr Thr His Met Ala Ile His Thr Gly Glu Lys Arg Tyr Lys
    210                 215                 220

Cys Asn Glu Cys Gly Lys Val Phe Arg Gln Ser Ser Asn Leu Ala Ser
225                 230                 235                 240

His His Arg Met His Thr Gly Glu Lys Pro Tyr Lys
             245                 250
```

```
<210>  13
<211>  8588
<212>  DNA
<213>  Human

<400>  13
cgcggcccga gcgcctcttt tcgggattaa aagcgccgcc agctcccgcc gccgccgccg      60

tcgccagcag cgccgctgca gccgccgccg ccggagaagc aaccgctggg cggtgagatc     120

cccctagaca tgcggctcgg gggcgggcag ctggtgtcag aggagctgat gaacctgggc     180

gagagcttca tccagaccaa cgacccgtcg ctgaagctct ccagtgcgc cgtctgcaac     240

aagttcacga cggacaacct ggacatgctg ggcctgcaca tgaacgtgga gcgcagcctg     300

tcggaggacg agtggaaggc ggtgatgggg gactcatacc agtgcaagct ctgccgctac     360

aacacccagc tcaaggccaa cttccagctg cactgcaaga cagacaagca cgtgcagaag     420

taccagctgg tggcccacat caaggagggc ggcaaggcca acgagtggag gctcaagtgt     480

gtggccatcg gcaacccgt gcacctcaag tgcaacgcct gtgactacta caccaacagc     540

ctggagaagc tgcggctgca cacggtcaac tccaggcacg aggccagcct gaagttgtac     600
```

```
aagcacctgc agcagcatga gagtggtgta gaaggtgaga gctgctacta ccactgcgtt      660

ctgtgcaact actccaccaa ggccaagctc aacctcatcc agcatgtgcg ctccatgaag      720

caccagcgaa gcgagagcct gcgaaagctg cagcggctgc agaagggcct tccagaggag      780

gacgaggacc tggggcagat cttcaccatc cgcaggtgcc cctccacgga cccagaagaa      840

gccattgaag atgttgaagg acccagtgaa acagctgctg atccagagga gcttgctaag      900

gaccaagagg gcggagcatc gtccagccaa gcagagaagg agctgacaga ttctcctgca      960

acctccaaac gcatctcctt cccaggtagc tcagagtctc ccctctcttc gaagcgacca     1020

aaaacagctg aggagatcaa accggagcag atgtaccagt gtccctactg caagtacagt     1080

aatgccgatg tcaaccggct ccgggtgcat gccatgacgc agcactcggt gcaacccatg     1140

cttcgctgcc ccctgtgcca ggacatgctc aacaacaaga tccacctcca gctgcacctc     1200

acccacctcc acagcgtggc acctgactgc gtggagaagc tcattatgac ggtgaccacc     1260

cctgagatgg tgatgccaag cagcatgttc ctcccagcag ctgttccaga tcgagatggg     1320

aattccaatt tggaagaggc aggaaagcag cctgaaacct cagaggatct gggaaagaac     1380

atcttgccat ccgcaagcac agagcaaagc ggagatttga aaccatcccc tgctgaccca     1440

ggctctgtga gagaagactc aggcttcatc tgctggaaga aggggtgcaa ccaggttttc     1500

aaaacttctg ctgcccttca gacgcatttt aatgaagtgc atgccaagag gcctcagctg     1560

ccggtgtcag atcgccatgt gtacaagtac cgctgtaatc agtgtagcct ggccttcaag     1620

accattgaaa agttgcagct ccattctcag taccatgtga tcagagctgc caccatgtgc     1680

tgtctttgtc agcgcagttt ccgaactttc caggctctga agaagcacct tgagacaagc     1740

cacctggagc tgagtgaggc tgacatccaa cagctttatg gtggcctgct ggccaatggg     1800

gacctcctgg caatgggaga ccccactctg gctgaggacc ataccataat tgttgaggaa     1860

gacaaggagg aagagagtga cttggaagat aaacagagcc caacgggcag tgactctggg     1920

tcagtacaag aagactcggg ctcagagcca aagagagctc tgcctttcag aaaaggtccc     1980

aattttacta tggaaaagtt cctagaccct tctcgccctt acaagtgtac cgtctgcaag     2040

gaatctttca ctcaaaagaa tatcctgcta gtacactaca attctgtctc ccacctgcat     2100

aagttaaaga gagcccttca agaatcagca accggtcagc cagaacccac cagcagccca     2160

gacaacaaac ctttaagtg taacacttgt aatgtggcct acagccagag ttccactctg     2220

gagatccata tgaggtctgt gttacatcaa accaaggccc gggcagccaa gctggaggct     2280

gcaagtggca gcagcaatgg gactgggaac agcagcagta tttccttgag ctcctccacg     2340

ccaagtcctg tgagcaccag tggcagtaac acctttacca cctccaatcc aagcagtgct     2400

ggcattgctc caagctctaa cttactaagc caagtgccca ctgagagtgt agggatgcca     2460
```

```
ccccctggggga  atcctattgg  tgccaacatt  gcttcccctt  cagagcccaa  agaggccaat    2520

cggaagaaac  tggcagatat  gattgcatcc  aggcagcagc  aacaacagca  gcagcaacag    2580

caacaacaac  aacaacaaca  acaacaacaa  gcacaaacgc  tgcccaggc   ccaggctcaa    2640

gttcaagctc  acctgcagca  ggagctgcag  caacaggctg  ccctgatcca  gtctcagctg    2700

tttaacccca  ccctccttcc  tcacttcccc  atgacaactg  agaccctgct  gcaactacag    2760

cagcagcagc  acctcctctt  ccctttctac  atccccagtg  ctgagttcca  gcttaacccc    2820

gaggtgagct  tgccagtgac  cagtggggca  ctgacactga  ctgggacagg  cccaggcctg    2880

ctggaagatc  tgaaggctca  ggttcaggtc  ccacagcaga  gccatcagca  gatcttgccg    2940

cagcagcagc  agaaccaact  ctctatagcc  cagagtcact  ctgccctcct  tcagccaagc    3000

cagcacccg   aaaagaagaa  caaattggtc  atcaaagaaa  aggaaaaga   aagccagaga    3060

gagagggaca  gcgccgaggg  gggagagggc  aacaccggtc  cgaaggaaac  actgccagat    3120

gccttgaagg  ccaaagagaa  gaaagagttg  gcaccagggg  gtggttctga  gccttccatg    3180

ctccctccac  gcattgcttc  agatgccaga  gggaacgcca  ccaaggccct  gctggagaac    3240

tttggctttg  agttggtcat  ccagtataat  gagaacaagc  agaaggtgca  gaaaaagaat    3300

gggaagactg  accagggaga  gaacctggaa  aagctcgagt  gtgactcctg  cggcaagttg    3360

ttttccaaca  tcttgatttt  aaagagtcat  caagagcacg  ttcatcagaa  ttactttcct    3420

ttcaaacagc  tcgagaggtt  tgccaaacag  tacagagacc  actacgataa  actgtaccca    3480

ctgaggcccc  agaccccaga  gccaccacca  cctccccctc  caccccctcc  accccactt    3540

ccggcagcgc  cgcctcagcc  ggcgtccaca  ccagccatcc  ccgcatcagc  cccacccatc    3600

acctcaccta  caattgcacc  ggcccagcca  tcagtgccgc  tcacccagct  ctccatgccg    3660

atggagctgc  ccatcttctc  gccgctgatg  atgcagacga  tgccgctgca  gaccttgccg    3720

gctcagctac  ccccgcagct  gggacctgtg  gagcctctgc  ctgcggacct  ggcccaactc    3780

taccagcatc  agctcaatcc  aaccctgctc  cagcagcaga  acaagaggcc  tcgcaccagg    3840

atcacagatg  atcagctccg  agtcttgcgg  caatattttg  acattaacaa  ctcccccagt    3900

gaagagcaaa  taaaagagat  ggcagacaag  tccgggttgc  cccagaaagt  gatcaagcac    3960

tggttcagga  acactctctt  caaagagagg  cagcgtaaca  aggactcccc  ttacaacttc    4020

agtaatcctc  ctatcaccag  cctggaggag  ctcaagattg  actcccggcc  cccttcgccg    4080

gaacctccaa  agcaggagta  ctggggaagc  aagaggtctt  caagaacaag  gtttacggac    4140

taccagctga  gggtcttaca  ggacttcttc  gatgccaatg  cttacccaaa  ggatgatgaa    4200

tttgagcaac  tctctaattt  actgaacctt  ccaacccgag  tgatagtggt  gtggtttcag    4260

aatgcccgac  agaaggccag  gaagaattat  gagaatcagg  gagagggcaa  agatggagag    4320

cggcgtgagc  ttacaaatga  tagatacatt  cgaacaagca  acttgaacta  ccagtgcaaa    4380
```

```
aaatgtagcc tggtgtttca gcgcatcttt gatctcatca agcaccagaa gaagctgtgt   4440

tacaaggatg aggatgagga ggggcaggac gacagccaaa atgaggattc catggatgcc   4500

atggaaatcc tgacgcctac cagctcatcc tgcagtaccc cgatgccctc acaggcttac   4560

agcgccccag caccatcagc caataataca gcttcctccg ctttcttgca gcttacagcg   4620

gaggctgagg aactggccac cttcaattca aaaacagagg caggcgatga gaaaccaaag   4680

ctggcggaag ctcccagtgc acagccaaac caaacccaag aaaagcaagg acaaccaaag   4740

ccagagctgc agcagcaaga gcagcccgag cagaagacca acactcccca gcagaagctc   4800

ccccagctgg tgtccctgcc ttcgttgcca cagcctcctc acaagcgcc  ccctccacag    4860

tgccccttac cccagtcgag ccccagtcct tcccagctct cccacctgcc cctcaagccc   4920

ctccacacat caactcctca acagctcgca aacctacctc ctcagctaat cccctaccag   4980

tgtgaccagt gtaagttggc atttccgtca tttgagcact ggcaggagca tcagcagctc   5040

cacttcctga gcgcgcagaa ccagttcatc caccccagt ttttggacag gtccctggat    5100

atgccttca tgctctttga tcccagtaac ccactcctgg ccagccagct gctctctggg    5160

gccatacctc agattccagc aagctcagcc acttctcctt caactccaac ctccacaatg   5220

aacactctca agaggaagct ggaggaaaag gccagtgcaa gccctggcga aaacgacagt   5280

gggacaggag gagaagagcc tcagagagac aagcgtttga gaacaaccat cacaccggaa   5340

caactagaaa ttctctacca gaagtatcta ctggattcca atccgactcg aaagatgttg   5400

gatcacattg cacacgaggt gggcttgaag aaacgtgtgg tacaagtctg gtttcagaac   5460

acccgagctc gggaaaggaa aggacagttc cgggctgtag gcccagcgca ggcccacagg   5520

agatgccctt tttgcagagc gctcttcaaa gccaagactg ctcttgaggc tcatatccgg   5580

tcccgtcact ggcatgaagc caagagagct ggctacaacc taactctgtc tgcgatgctc   5640

ttagactgtg atggggggact ccagatgaaa ggagatattt ttgacggaac tagcttttcc   5700

cacctacccc caagcagtag tgatggtcag ggtgtccccc tctcacctgt gagtaaaacc   5760

atggaattgt cacccagaac tcttctaagc ccttcctcca ttaaggtgga agggattgaa   5820

gactttgaaa gcccctccat gtcctcagtt aatctaaact ttgaccaaac taagctggac   5880

aacgatgact gttcctctgt caacacagca atcacagata ccacaactgg agacgagggc   5940

aacgcagata cgacagtgc aacgggaata gcaactgaaa ccaaatcctc ttctgcaccc    6000

aacgaagggt tgaccaaagc ggccatgatg gcaatgtctg agtatgaaga tcggttgtca   6060

tctggtctgg tcagcccggc cccgagcttt tatagcaagg aatatgacaa tgaaggtaca   6120

gtggactaca gtgaaacctc aagccttgca gatccctgct ccccgagtcc tggtgcgagt   6180

ggatctgcag gcaaatctgg tgacagcggg gatcggcctg ggcagaaacg ttttcgcact   6240
```

```
caaatgacca atctgcagct gaaggtcctc aagtcatgct ttaatgacta caggacaccc    6300

actatgctag aatgtgaggt cctgggcaat gacattggac tgccaaagag agtcgttcag    6360

gtctggttcc agaatgcccg ggcaaaagaa aagaagtcca agttaagcat ggccaagcat    6420

tttggtataa accaaacgag ttatgaggga cccaaaacag agtgcacttt gtgtggcatc    6480

aagtacagcg ctcggctgtc tgtacgtgac catatctttt cccaacagca tatctccaaa    6540

gttaaagaca ccattggaag ccagctggac aaggagaaag aatactttga cccagccacc    6600

gtacgtcagt tgatggctca acaagagttg gaccggatta aaaaggccaa cgaggtcctt    6660

ggactggcag ctcagcagca agggatgttt gacaacaccc ctcttcaggc ccttaacctt    6720

cctacagcat atccagcgct ccagggcatt cctcctgtgt tgctcccggg cctcaacagc    6780

ccctccttgc caggctttac tccatccaac acagctttaa cgtctcctaa gccgaacttg    6840

atgggtctgc ccagcacaac tgttccttcc cctggcctcc ccacttctgg attaccaaat    6900

aaaccgtcct cagcgtcgct gagctcccca accccagcac aagccacgat ggcgatgggc    6960

cctcagcaac ccccccagca gcagcagcag cagcagcaac cacaggtgca gcagcctccc    7020

ccgccgccag cagcccagcc gccacccaca ccacagctcc cactgcaaca gcagcagcaa    7080

cgcaaggaca aagacagtga gaaagtaaag gagaaggaaa aggcacacaa agggaaaggg    7140

gaacccctgc ctgtccccaa gaaggagaaa ggagaggccc ccacggcaac tgcagccacg    7200

atctcagccc cgctgcccac catggagtat gcggtagacc ctgcacagct gcaggccctg    7260

caggccgcgt tgacttcgga ccccacagca ttgctcacaa gccagttcct tccttacttt    7320

gtaccaggct tttctcctta ttatgctccc cagatccctg cgccctgca gagcgggtac    7380

ctgcagccta tgtatggcat ggaaggcctg ttcccctaca gccctgcact gtcgcaggcc    7440

ctgatggggc tgtccccagg ctccctactg cagcagtacc agcaatacca gcagagtctg    7500

caggaggcaa ttcagcagca gcagcagcaa aaagtgcagc agcagcagcc caaagcaagc    7560

caaaccccag tcccccccgg ggctccttcc ccagacaaag accctgccaa agaatccccc    7620

aaaccagaag aacagaaaaa caccccccgt gaggtgtccc ccctcctgcc gaaactccct    7680

gaagagccag aagcagaaag caaaagtgcg gactccctct acgacccctt cattgttcca    7740

aaggtgcagt acaagttggt ctgccgcaag tgccaggcgg gcttcagcga cgaggaggca    7800

gcgaggagcc acctgaagtc cctctgcttc ttcggccagt ctgtggtgaa cctgcaagag    7860

atggtgcttc acgtccccac cggcggcggc ggcggtggca gtggcggcgg cggcggcggt    7920

ggcggcggcg gcggcggcgg cggcggcggc tcgtaccact gcctggcgtg cgagagcgcg    7980

ctctgtgggg aggaagctct gagtcaacat ctcgagtcgg ccttgcacaa acacagaaca    8040

atcacgagag cagcaagaaa cgccaaagag caccctagtt tattacctca ctctgcctgc    8100

ttccccgatc ctagcaccgc atctacctcg cagtctgccg ctcactcaaa cgacagcccc    8160
```

```
cctcccccgt cggccgccgc cccctcctcc gcttcccccc acgcctccag gaagtcttgg    8220

ccgcaagtgg tctcccgggc ttcggcagcg aagccccctt cttttcctcc tctctcctca    8280

tcttcaacgg ttacctcaag ttcatgcagc acctcagggg ttcagccctc gatgccaaca    8340

gacgactatt cggaggagtc tgacacggat ctcagccaaa agtccgacgg accggcgagc    8400

ccggtggagg gtcccaaaga ccccagctgc cccaaggaca gtggtctgac cagtgtagga    8460

acggacacct tcagattgta agctttgaag atgaacaata caaacaaatg aatttaaata    8520

caaaaattaa taacaaacca atttcaaaaa tagactaact gcaattccaa agcttctaac    8580

caaaaaac                                                             8588
```

<210> 14
<211> 2783
<212> PRT
<213> Human

<400> 14

```
Met Arg Leu Gly Gly Gly Gln Leu Val Ser Glu Glu Leu Met Asn Leu
1               5                   10                  15


Gly Glu Ser Phe Ile Gln Thr Asn Asp Pro Ser Leu Lys Leu Phe Gln
            20                  25                  30


Cys Ala Val Cys Asn Lys Phe Thr Thr Asp Asn Leu Asp Met Leu Gly
        35                  40                  45


Leu His Met Asn Val Glu Arg Ser Leu Ser Glu Asp Glu Trp Lys Ala
    50                  55                  60


Val Met Gly Asp Ser Tyr Gln Cys Lys Leu Cys Arg Tyr Asn Thr Gln
65                  70                  75                  80


Leu Lys Ala Asn Phe Gln Leu His Cys Lys Thr Asp Lys His Val Gln
                85                  90                  95


Lys Tyr Gln Leu Val Ala His Ile Lys Glu Gly Gly Lys Ala Asn Glu
            100                 105                 110


Trp Arg Leu Lys Cys Val Ala Ile Gly Asn Pro Val His Leu Lys Cys
        115                 120                 125


Asn Ala Cys Asp Tyr Tyr Thr Asn Ser Leu Glu Lys Leu Arg Leu His
    130                 135                 140


Thr Val Asn Ser Arg His Glu Ala Ser Leu Lys Leu Tyr Lys His Leu
145                 150                 155                 160
```

Page 14

```
Gln Gln His Glu Ser Gly Val Glu Gly Glu Ser Cys Tyr Tyr His Cys
                165                 170             175

Val Leu Cys Asn Tyr Ser Thr Lys Ala Lys Leu Asn Leu Ile Gln His
            180             185             190

Val Arg Ser Met Lys His Gln Arg Ser Glu Ser Leu Arg Lys Leu Gln
            195             200             205

Arg Leu Gln Lys Gly Leu Pro Glu Glu Asp Glu Asp Leu Gly Gln Ile
    210             215             220

Phe Thr Ile Arg Arg Cys Pro Ser Thr Asp Pro Glu Glu Ala Ile Glu
225             230             235             240

Asp Val Glu Gly Pro Ser Glu Thr Ala Ala Asp Pro Glu Glu Leu Ala
            245             250             255

Lys Asp Gln Glu Gly Gly Ala Ser Ser Ser Gln Ala Glu Lys Glu Leu
            260             265             270

Thr Asp Ser Pro Ala Thr Ser Lys Arg Ile Ser Phe Pro Gly Ser Ser
            275             280             285

Glu Ser Pro Leu Ser Ser Lys Arg Pro Lys Thr Ala Glu Glu Ile Lys
    290             295             300

Pro Glu Gln Met Tyr Gln Cys Pro Tyr Cys Lys Tyr Ser Asn Ala Asp
305             310             315             320

Val Asn Arg Leu Arg Val His Ala Met Thr Gln His Ser Val Gln Pro
            325             330             335

Met Leu Arg Cys Pro Leu Cys Gln Asp Met Leu Asn Asn Lys Ile His
            340             345             350

Leu Gln Leu His Leu Thr His Leu His Ser Val Ala Pro Asp Cys Val
            355             360             365

Glu Lys Leu Ile Met Thr Val Thr Thr Pro Glu Met Val Met Pro Ser
    370             375             380

Ser Met Phe Leu Pro Ala Ala Val Pro Asp Arg Asp Gly Asn Ser Asn
385             390             395             400

Leu Glu Glu Ala Gly Lys Gln Pro Glu Thr Ser Glu Asp Leu Gly Lys
```

```
                    405                     410                     415

Asn Ile Leu Pro Ser Ala Ser Thr Glu Gln Ser Gly Asp Leu Lys Pro
            420                 425                 430

Ser Pro Ala Asp Pro Gly Ser Val Arg Glu Asp Ser Gly Phe Ile Cys
            435                 440                 445

Trp Lys Lys Gly Cys Asn Gln Val Phe Lys Thr Ser Ala Ala Leu Gln
    450                 455                 460

Thr His Phe Asn Glu Val His Ala Lys Arg Pro Gln Leu Pro Val Ser
465                 470                 475                 480

Asp Arg His Val Tyr Lys Tyr Arg Cys Asn Gln Cys Ser Leu Ala Phe
                485                 490                 495

Lys Thr Ile Glu Lys Leu Gln Leu His Ser Gln Tyr His Val Ile Arg
            500                 505                 510

Ala Ala Thr Met Cys Cys Leu Cys Gln Arg Ser Phe Arg Thr Phe Gln
            515                 520                 525

Ala Leu Lys Lys His Leu Glu Thr Ser His Leu Glu Leu Ser Glu Ala
            530                 535                 540

Asp Ile Gln Gln Leu Tyr Gly Gly Leu Leu Ala Asn Gly Asp Leu Leu
545                 550                 555                 560

Ala Met Gly Asp Pro Thr Leu Ala Glu Asp His Thr Ile Ile Val Glu
                565                 570                 575

Glu Asp Lys Glu Glu Glu Ser Asp Leu Glu Asp Lys Gln Ser Pro Thr
            580                 585                 590

Gly Ser Asp Ser Gly Ser Val Gln Glu Asp Ser Gly Ser Glu Pro Lys
            595                 600                 605

Arg Ala Leu Pro Phe Arg Lys Gly Pro Asn Phe Thr Met Glu Lys Phe
    610                 615                 620

Leu Asp Pro Ser Arg Pro Tyr Lys Cys Thr Val Cys Lys Glu Ser Phe
625                 630                 635                 640

Thr Gln Lys Asn Ile Leu Leu Val His Tyr Asn Ser Val Ser His Leu
                645                 650                 655
```

Page 16

```
His Lys Leu Lys Arg Ala Leu Gln Glu Ser Ala Thr Gly Gln Pro Glu
        660             665             670

Pro Thr Ser Ser Pro Asp Asn Lys Pro Phe Lys Cys Asn Thr Cys Asn
        675             680             685

Val Ala Tyr Ser Gln Ser Ser Thr Leu Glu Ile His Met Arg Ser Val
    690             695             700

Leu His Gln Thr Lys Ala Arg Ala Ala Lys Leu Glu Ala Ala Ser Gly
705             710             715                     720

Ser Ser Asn Gly Thr Gly Asn Ser Ser Ser Ile Ser Leu Ser Ser Ser
            725             730             735

Thr Pro Ser Pro Val Ser Thr Ser Gly Ser Asn Thr Phe Thr Thr Ser
            740             745             750

Asn Pro Ser Ser Ala Gly Ile Ala Pro Ser Ser Asn Leu Leu Ser Gln
            755             760             765

Val Pro Thr Glu Ser Val Gly Met Pro Pro Leu Gly Asn Pro Ile Gly
    770             775             780

Ala Asn Ile Ala Ser Pro Ser Glu Pro Lys Glu Ala Asn Arg Lys Lys
785             790             795                     800

Leu Ala Asp Met Ile Ala Ser Arg Gln Gln Gln Gln Gln Gln Gln Gln
            805             810             815

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala Gln Thr Leu Ala
        820             825             830

Gln Ala Gln Ala Gln Val Gln Ala His Leu Gln Gln Glu Leu Gln Gln
        835             840             845

Gln Ala Ala Leu Ile Gln Ser Gln Leu Phe Asn Pro Thr Leu Leu Pro
    850             855             860

His Phe Pro Met Thr Thr Glu Thr Leu Leu Gln Leu Gln Gln Gln Gln
865             870             875             880

His Leu Leu Phe Pro Phe Tyr Ile Pro Ser Ala Glu Phe Gln Leu Asn
            885             890             895

Pro Glu Val Ser Leu Pro Val Thr Ser Gly Ala Leu Thr Leu Thr Gly
            900             905             910
```

```
Thr Gly Pro Gly Leu Leu Glu Asp Leu Lys Ala Gln Val Gln Val Pro
        915                 920                 925

Gln Gln Ser His Gln Gln Ile Leu Pro Gln Gln Gln Gln Asn Gln Leu
    930                 935                 940

Ser Ile Ala Gln Ser His Ser Ala Leu Leu Gln Pro Ser Gln His Pro
945                 950                 955                 960

Glu Lys Lys Asn Lys Leu Val Ile Lys Glu Lys Glu Lys Glu Ser Gln
                965                 970                 975

Arg Glu Arg Asp Ser Ala Glu Gly Gly Glu Gly Asn Thr Gly Pro Lys
            980                 985                 990

Glu Thr Leu Pro Asp Ala Leu Lys  Ala Lys Glu Lys Lys  Glu Leu Ala
        995                 1000                1005

Pro Gly  Gly Gly Ser Glu Pro  Ser Met Leu Pro Pro  Arg Ile Ala
    1010                1015                1020

Ser Asp  Ala Arg Gly Asn Ala  Thr Lys Ala Leu Leu  Glu Asn Phe
    1025                1030                1035

Gly Phe  Glu Leu Val Ile Gln  Tyr Asn Glu Asn Lys  Gln Lys Val
    1040                1045                1050

Gln Lys  Lys Asn Gly Lys Thr  Asp Gln Gly Glu Asn  Leu Glu Lys
    1055                1060                1065

Leu Glu  Cys Asp Ser Cys Gly  Lys Leu Phe Ser Asn  Ile Leu Ile
    1070                1075                1080

Leu Lys  Ser His Gln Glu His  Val His Gln Asn Tyr  Phe Pro Phe
    1085                1090                1095

Lys Gln  Leu Glu Arg Phe Ala  Lys Gln Tyr Arg Asp  His Tyr Asp
    1100                1105                1110

Lys Leu  Tyr Pro Leu Arg Pro  Gln Thr Pro Glu Pro  Pro Pro Pro
    1115                1120                1125

Pro Pro  Pro Pro Pro Pro Pro  Pro Leu Pro Ala Ala  Pro Pro Gln
    1130                1135                1140

Pro Ala  Ser Thr Pro Ala Ile  Pro Ala Ser Ala Pro  Pro Ile Thr
    1145                1150                1155
```

Ser Pro  Thr Ile Ala Pro Ala  Gln Pro Ser Val Pro  Leu Thr Gln
    1160                1165                1170

Leu Ser  Met Pro Met Glu Leu  Pro Ile Phe Ser Pro  Leu Met Met
    1175                1180                1185

Gln Thr  Met Pro Leu Gln Thr  Leu Pro Ala Gln Leu  Pro Pro Gln
    1190                1195                1200

Leu Gly  Pro Val Glu Pro Leu  Pro Ala Asp Leu Ala  Gln Leu Tyr
    1205                1210                1215

Gln His  Gln Leu Asn Pro Thr  Leu Leu Gln Gln Gln  Asn Lys Arg
    1220                1225                1230

Pro Arg  Thr Arg Ile Thr Asp  Asp Gln Leu Arg Val  Leu Arg Gln
    1235                1240                1245

Tyr Phe  Asp Ile Asn Asn Ser  Pro Ser Glu Glu Gln  Ile Lys Glu
    1250                1255                1260

Met Ala  Asp Lys Ser Gly Leu  Pro Gln Lys Val Ile  Lys His Trp
    1265                1270                1275

Phe Arg  Asn Thr Leu Phe Lys  Glu Arg Gln Arg Asn  Lys Asp Ser
    1280                1285                1290

Pro Tyr  Asn Phe Ser Asn Pro  Pro Ile Thr Ser Leu  Glu Glu Leu
    1295                1300                1305

Lys Ile  Asp Ser Arg Pro Pro  Ser Pro Glu Pro Pro  Lys Gln Glu
    1310                1315                1320

Tyr Trp  Gly Ser Lys Arg Ser  Ser Arg Thr Arg Phe  Thr Asp Tyr
    1325                1330                1335

Gln Leu  Arg Val Leu Gln Asp  Phe Phe Asp Ala Asn  Ala Tyr Pro
    1340                1345                1350

Lys Asp  Asp Glu Phe Glu Gln  Leu Ser Asn Leu Leu  Asn Leu Pro
    1355                1360                1365

Thr Arg  Val Ile Val Val Trp  Phe Gln Asn Ala Arg  Gln Lys Ala
    1370                1375                1380

Arg Lys  Asn Tyr Glu Asn Gln  Gly Glu Gly Lys Asp  Gly Glu Arg

```
        1385                    1390                    1395

Arg Glu  Leu Thr Asn Asp Arg  Tyr Ile Arg Thr Ser  Asn Leu Asn
         1400                   1405                  1410

Tyr Gln  Cys Lys Lys Cys Ser  Leu Val Phe Gln Arg  Ile Phe Asp
         1415                   1420                  1425

Leu Ile  Lys His Gln Lys Lys  Leu Cys Tyr Lys Asp  Glu Asp Glu
         1430                   1435                  1440

Glu Gly  Gln Asp Asp Ser Gln  Asn Glu Asp Ser Met  Asp Ala Met
         1445                   1450                  1455

Glu Ile  Leu Thr Pro Thr Ser  Ser Ser Cys Ser Thr  Pro Met Pro
         1460                   1465                  1470

Ser Gln  Ala Tyr Ser Ala Pro  Ala Pro Ser Ala Asn  Asn Thr Ala
         1475                   1480                  1485

Ser Ser  Ala Phe Leu Gln Leu  Thr Ala Glu Ala Glu  Glu Leu Ala
         1490                   1495                  1500

Thr Phe  Asn Ser Lys Thr Glu  Ala Gly Asp Glu Lys  Pro Lys Leu
         1505                   1510                  1515

Ala Glu  Ala Pro Ser Ala Gln  Pro Asn Gln Thr Gln  Glu Lys Gln
         1520                   1525                  1530

Gly Gln  Pro Lys Pro Glu Leu  Gln Gln Gln Glu Gln  Pro Glu Gln
         1535                   1540                  1545

Lys Thr  Asn Thr Pro Gln Gln  Lys Leu Pro Gln Leu  Val Ser Leu
         1550                   1555                  1560

Pro Ser  Leu Pro Gln Pro Pro  Pro Gln Ala Pro Pro  Pro Gln Cys
         1565                   1570                  1575

Pro Leu  Pro Gln Ser Ser Pro  Ser Pro Ser Gln Leu  Ser His Leu
         1580                   1585                  1590

Pro Leu  Lys Pro Leu His Thr  Ser Thr Pro Gln Gln  Leu Ala Asn
         1595                   1600                  1605

Leu Pro  Pro Gln Leu Ile Pro  Tyr Gln Cys Asp Gln  Cys Lys Leu
         1610                   1615                  1620
```

```
Ala Phe  Pro Ser Phe Glu His  Trp Gln Glu His Gln  Gln Leu His
    1625             1630             1635

Phe Leu  Ser Ala Gln Asn Gln  Phe Ile His Pro Gln  Phe Leu Asp
    1640             1645             1650

Arg Ser  Leu Asp Met Pro Phe  Met Leu Phe Asp Pro  Ser Asn Pro
    1655             1660             1665

Leu Leu  Ala Ser Gln Leu Leu  Ser Gly Ala Ile Pro  Gln Ile Pro
    1670             1675             1680

Ala Ser  Ser Ala Thr Ser Pro  Ser Thr Pro Thr Ser  Thr Met Asn
    1685             1690             1695

Thr Leu  Lys Arg Lys Leu Glu  Glu Lys Ala Ser Ala  Ser Pro Gly
    1700             1705             1710

Glu Asn  Asp Ser Gly Thr Gly  Gly Glu Glu Pro Gln  Arg Asp Lys
    1715             1720             1725

Arg Leu  Arg Thr Thr Ile Thr  Pro Glu Gln Leu Glu  Ile Leu Tyr
    1730             1735             1740

Gln Lys  Tyr Leu Leu Asp Ser  Asn Pro Thr Arg Lys  Met Leu Asp
    1745             1750             1755

His Ile  Ala His Glu Val Gly  Leu Lys Lys Arg Val  Val Gln Val
    1760             1765             1770

Trp Phe  Gln Asn Thr Arg Ala  Arg Glu Arg Lys Gly  Gln Phe Arg
    1775             1780             1785

Ala Val  Gly Pro Ala Gln Ala  His Arg Arg Cys Pro  Phe Cys Arg
    1790             1795             1800

Ala Leu  Phe Lys Ala Lys Thr  Ala Leu Glu Ala His  Ile Arg Ser
    1805             1810             1815

Arg His  Trp His Glu Ala Lys  Arg Ala Gly Tyr Asn  Leu Thr Leu
    1820             1825             1830

Ser Ala  Met Leu Leu Asp Cys  Asp Gly Gly Leu Gln  Met Lys Gly
    1835             1840             1845

Asp Ile  Phe Asp Gly Thr Ser  Phe Ser His Leu Pro  Pro Ser Ser
    1850             1855             1860
```

```
Ser Asp Gly Gln Gly Val Pro Leu Ser Pro Val Ser Lys Thr Met
    1865                1870                1875

Glu Leu Ser Pro Arg Thr Leu Leu Ser Pro Ser Ser Ile Lys Val
    1880                1885                1890

Glu Gly Ile Glu Asp Phe Glu Ser Pro Ser Met Ser Ser Val Asn
    1895                1900                1905

Leu Asn Phe Asp Gln Thr Lys Leu Asp Asn Asp Asp Cys Ser Ser
    1910                1915                1920

Val Asn Thr Ala Ile Thr Asp Thr Thr Thr Gly Asp Glu Gly Asn
    1925                1930                1935

Ala Asp Asn Asp Ser Ala Thr Gly Ile Ala Thr Glu Thr Lys Ser
    1940                1945                1950

Ser Ser Ala Pro Asn Glu Gly Leu Thr Lys Ala Ala Met Met Ala
    1955                1960                1965

Met Ser Glu Tyr Glu Asp Arg Leu Ser Ser Gly Leu Val Ser Pro
    1970                1975                1980

Ala Pro Ser Phe Tyr Ser Lys Glu Tyr Asp Asn Glu Gly Thr Val
    1985                1990                1995

Asp Tyr Ser Glu Thr Ser Ser Leu Ala Asp Pro Cys Ser Pro Ser
    2000                2005                2010

Pro Gly Ala Ser Gly Ser Ala Gly Lys Ser Gly Asp Ser Gly Asp
    2015                2020                2025

Arg Pro Gly Gln Lys Arg Phe Arg Thr Gln Met Thr Asn Leu Gln
    2030                2035                2040

Leu Lys Val Leu Lys Ser Cys Phe Asn Asp Tyr Arg Thr Pro Thr
    2045                2050                2055

Met Leu Glu Cys Glu Val Leu Gly Asn Asp Ile Gly Leu Pro Lys
    2060                2065                2070

Arg Val Val Gln Val Trp Phe Gln Asn Ala Arg Ala Lys Glu Lys
    2075                2080                2085

Lys Ser Lys Leu Ser Met Ala Lys His Phe Gly Ile Asn Gln Thr
    2090                2095                2100
```

```
Ser Tyr  Glu Gly Pro Lys Thr  Glu Cys Thr Leu Cys  Gly Ile Lys
    2105             2110             2115

Tyr Ser  Ala Arg Leu Ser Val  Arg Asp His Ile Phe  Ser Gln Gln
    2120             2125             2130

His Ile  Ser Lys Val Lys Asp  Thr Ile Gly Ser Gln  Leu Asp Lys
    2135             2140             2145

Glu Lys  Glu Tyr Phe Asp Pro  Ala Thr Val Arg Gln  Leu Met Ala
    2150             2155             2160

Gln Gln  Glu Leu Asp Arg Ile  Lys Lys Ala Asn Glu  Val Leu Gly
    2165             2170             2175

Leu Ala  Ala Gln Gln Gln Gly  Met Phe Asp Asn Thr  Pro Leu Gln
    2180             2185             2190

Ala Leu  Asn Leu Pro Thr Ala  Tyr Pro Ala Leu Gln  Gly Ile Pro
    2195             2200             2205

Pro Val  Leu Leu Pro Gly Leu  Asn Ser Pro Ser Leu  Pro Gly Phe
    2210             2215             2220

Thr Pro  Ser Asn Thr Ala Leu  Thr Ser Pro Lys Pro  Asn Leu Met
    2225             2230             2235

Gly Leu  Pro Ser Thr Thr Val  Pro Ser Pro Gly Leu  Pro Thr Ser
    2240             2245             2250

Gly Leu  Pro Asn Lys Pro Ser  Ser Ala Ser Leu Ser  Ser Pro Thr
    2255             2260             2265

Pro Ala  Gln Ala Thr Met Ala  Met Gly Pro Gln Gln  Pro Pro Gln
    2270             2275             2280

Gln Gln  Gln Gln Gln Gln Gln  Pro Gln Val Gln Gln  Pro Pro Pro
    2285             2290             2295

Pro Pro  Ala Ala Gln Pro Pro  Pro Thr Pro Gln Leu  Pro Leu Gln
    2300             2305             2310

Gln Gln  Gln Gln Arg Lys Asp  Lys Asp Ser Glu Lys  Val Lys Glu
    2315             2320             2325

Lys Glu  Lys Ala His Lys Gly  Lys Gly Glu Pro Leu  Pro Val Pro
```

```
        2330                    2335                    2340


Lys Lys Glu Lys Gly Glu Ala  Pro Thr Ala Thr Ala  Ala Thr Ile
    2345                     2350                    2355


Ser Ala Pro Leu Pro Thr Met  Glu Tyr Ala Val Asp  Pro Ala Gln
    2360                     2365                    2370


Leu Gln Ala Leu Gln Ala Ala  Leu Thr Ser Asp Pro  Thr Ala Leu
    2375                     2380                    2385


Leu Thr Ser Gln Phe Leu Pro  Tyr Phe Val Pro Gly  Phe Ser Pro
    2390                     2395                    2400


Tyr Tyr Ala Pro Gln Ile Pro  Gly Ala Leu Gln Ser  Gly Tyr Leu
    2405                     2410                    2415


Gln Pro Met Tyr Gly Met Glu  Gly Leu Phe Pro Tyr  Ser Pro Ala
    2420                     2425                    2430


Leu Ser Gln Ala Leu Met Gly  Leu Ser Pro Gly Ser  Leu Leu Gln
    2435                     2440                    2445


Gln Tyr Gln Gln Tyr Gln Gln  Ser Leu Gln Glu Ala  Ile Gln Gln
    2450                     2455                    2460


Gln Gln Gln Gln Lys Val Gln  Gln Gln Gln Pro Lys  Ala Ser Gln
    2465                     2470                    2475


Thr Pro Val Pro Pro Gly Ala  Pro Ser Pro Asp Lys  Asp Pro Ala
    2480                     2485                    2490


Lys Glu Ser Pro Lys Pro Glu  Glu Gln Lys Asn Thr  Pro Arg Glu
    2495                     2500                    2505


Val Ser Pro Leu Leu Pro Lys  Leu Pro Glu Glu Pro  Glu Ala Glu
    2510                     2515                    2520


Ser Lys Ser Ala Asp Ser Leu  Tyr Asp Pro Phe Ile  Val Pro Lys
    2525                     2530                    2535


Val Gln Tyr Lys Leu Val Cys  Arg Lys Cys Gln Ala  Gly Phe Ser
    2540                     2545                    2550


Asp Glu Glu Ala Ala Arg Ser  His Leu Lys Ser Leu  Cys Phe Phe
    2555                     2560                    2565
```

```
Gly Gln  Ser Val Val Asn Leu  Gln Glu Met Val Leu  His Val Pro
    2570                2575                2580

Thr Gly  Gly Gly Gly Gly Gly  Ser Gly Gly Gly Gly  Gly Gly Gly
    2585                2590                2595

Gly Gly  Gly Gly Gly Gly Gly  Gly Gly Ser Tyr His  Cys Leu Ala
    2600                2605                2610

Cys Glu  Ser Ala Leu Cys Gly  Glu Glu Ala Leu Ser  Gln His Leu
    2615                2620                2625

Glu Ser  Ala Leu His Lys His  Arg Thr Ile Thr Arg  Ala Ala Arg
    2630                2635                2640

Asn Ala  Lys Glu His Pro Ser  Leu Leu Pro His Ser  Ala Cys Phe
    2645                2650                2655

Pro Asp  Pro Ser Thr Ala Ser  Thr Ser Gln Ser Ala  Ala His Ser
    2660                2665                2670

Asn Asp  Ser Pro Pro Pro Pro  Ser Ala Ala Ala Pro  Ser Ser Ala
    2675                2680                2685

Ser Pro  His Ala Ser Arg Lys  Ser Trp Pro Gln Val  Val Ser Arg
    2690                2695                2700

Ala Ser  Ala Ala Lys Pro Pro  Ser Phe Pro Pro Leu  Ser Ser Ser
    2705                2710                2715

Ser Thr  Val Thr Ser Ser Ser  Cys Ser Thr Ser Gly  Val Gln Pro
    2720                2725                2730

Ser Met  Pro Thr Asp Asp Tyr  Ser Glu Glu Ser Asp  Thr Asp Leu
    2735                2740                2745

Ser Gln  Lys Ser Asp Gly Pro  Ala Ser Pro Val Glu  Gly Pro Lys
    2750                2755                2760

Asp Pro  Ser Cys Pro Lys Asp  Ser Gly Leu Thr Ser  Val Gly Thr
    2765                2770                2775

Asp Thr  Phe Arg Leu
    2780


<210>  15
<211>  30
<212>  DNA
```

<213>    Artificial Sequence

<220>
<223>    synthetic

<400>    15
agatcttaag cagaaatgat tgcaccattg                                30


<210>    16
<211>    28
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    synthetic

<400>    16
gtagataaag gtgtgtgtca ctgagctc                                 28


<210>    17
<211>    19
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    synthetic

<400>    17
ttggggttat tcgcaacgg                                           19


<210>    18
<211>    35
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    synthetic

<400>    18
gaactggatc cctgctcata taccttgtct cgatg                         35


<210>    19
<211>    26
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    synthetic

<400>    19
gaactggatc caccaaggac tccatg                                   26


<210>    20
<211>    18
<212>    DNA
<213>    Artificial Sequence

<220>

<223>  synthetic

<400>  20
cggaattagc ttggctgc                                                    18